Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

1 - 15. (canceled)

16. (new) A method of analyzing a target nucleic acid, comprising:

designing a first probe array comprising a plurality of probes complementary to a region of a reference genome of a first species;

hybridizing the target nucleic acid to the first probe array, wherein the target nucleic acid is derived from a target genome of a second species;

estimating the sequence of said target nucleic acid;

designing a second probe array comprising a plurality of probes complementary to the estimated sequence of the target nucleic acid; and

reestimating the sequence of said target nucleic acid.

17. (new) The method of Claim 16 wherein the region of a reference genome comprises at least 10% of the genome.

18. (new) The method of Claim 17 wherein the region of a reference genome comprises the whole genome.

19. (new) The method of Claim 18 wherein the target genome shows 50-99% sequence identity with the reference genome.

20. (new) The method of Claim 19 wherein the reference genome is from a human and the target genome is from a primate.

21. (new) The method of Claim 19 wherein the probe arrays comprise probes tiling both strands of the reference genome.

22. (new) The method of Claim 19 wherein the probe arrays comprise duplicate arrays.

23. (new) The method of Claim 22 wherein one of the duplicate arrays is hybridized at a lower stringency with respect to the other duplicate array.

24. (new) The method of Claim 16 wherein the hybridizing comprises hybridizing a nucleic acid sample representing the whole genome.

25. (new) The method of Claim 24 wherein the hybridizing comprises hybridizing pools of 1 Mb sequences of the genome.

26. (new) A method of identifying a plurality of functionally important elements of a genome comprising:

(a) identifying a known functionally important region in a known reference genome;

(b) performing iterative sequencing on a variant genomic sample to obtain a reestimated sequence of the variant genomic sample wherein the restimated sequence is a subset of the known functionally important region of the reference genome; and

(c) deeming a region in the variant genomic sample to be conserved with the known functionally important region of the reference genome if the reestimated sequence is constant between at least two successive sequencing cycles.

27. (new) The method of Claim 26 wherein the functionally important element is an exon.

28. (new) The method of Claim 26 wherein the functionally important element is a regulatory element.

29. (new) The method of Claim 28 wherein the functionally important element is a promoter.